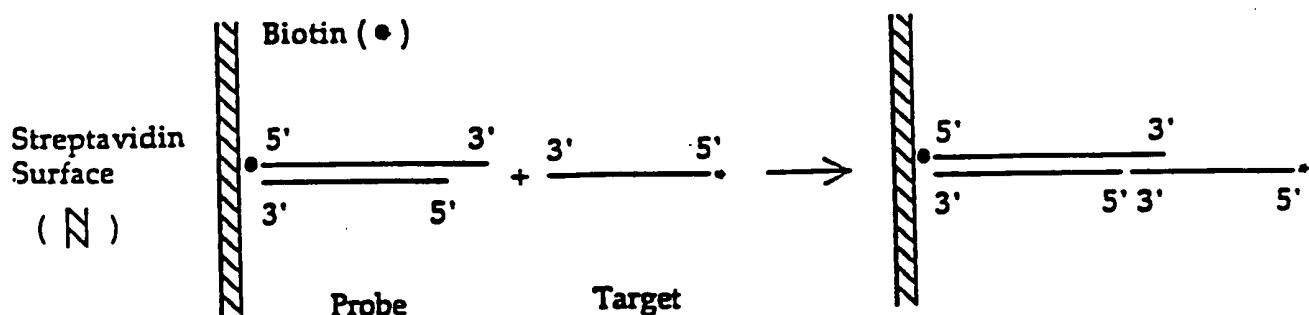
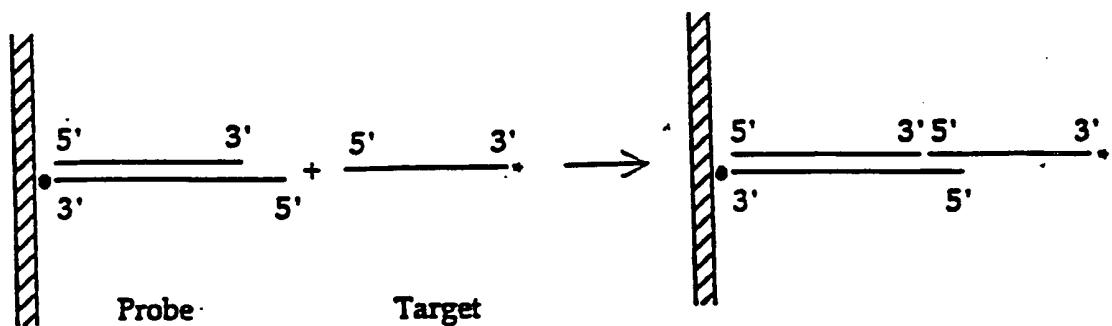


Nucleic Acid Structure	Calculated T_m ($^{\circ}\text{C}$, average base composition)			
	n = 8	7	6	5
— — — —	38	33	25	15
— — — — —	33	25	15	3
— — — — — —	25	15	3	-14
— — — — —	51	46	40	31
— — — — — —	46	40	31	21
— — — — — — —	40	31	21	11

FIGURE 1



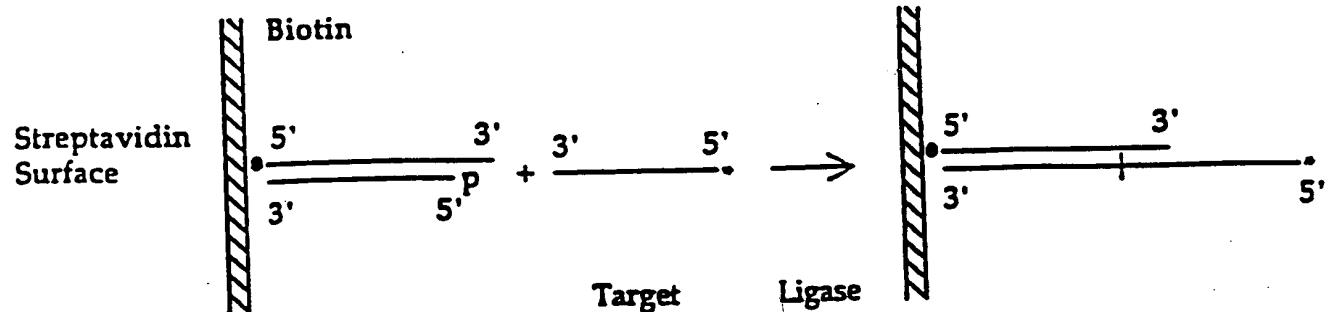
A. Basic scheme for positional SBH



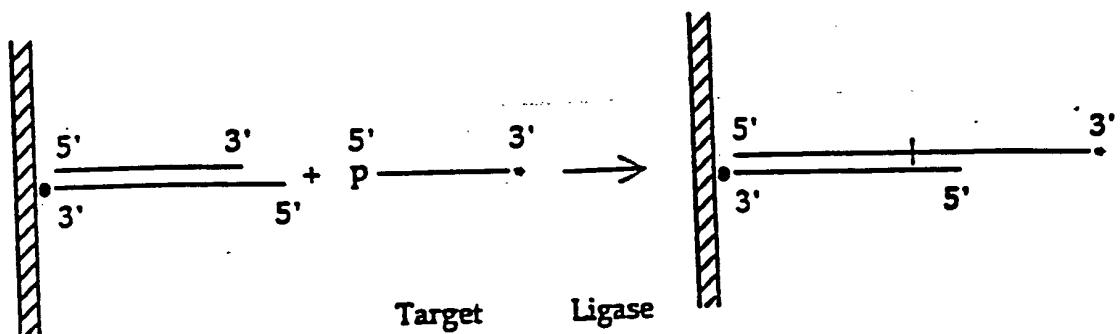
B. Alternate scheme

FIGURE 2

Ligation of target DNA with probe



A.



B.

FIGURE 3

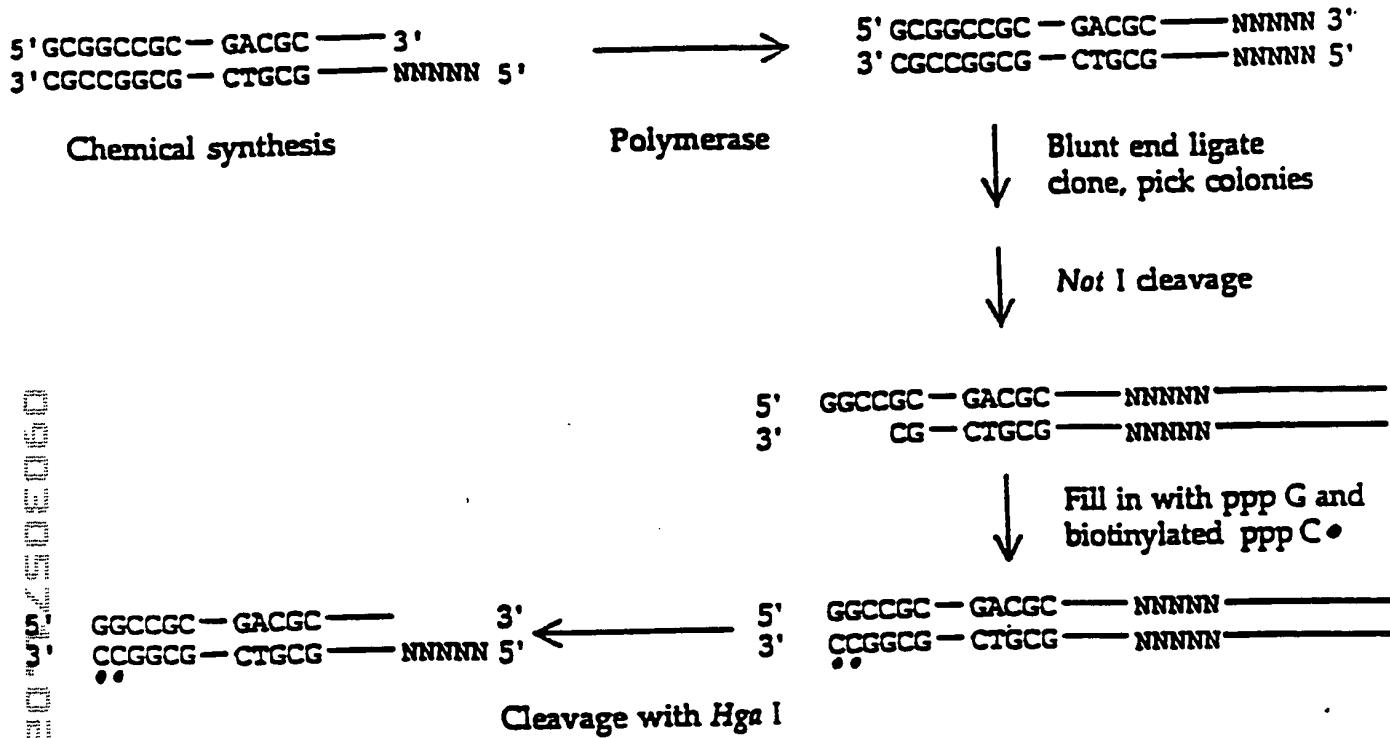
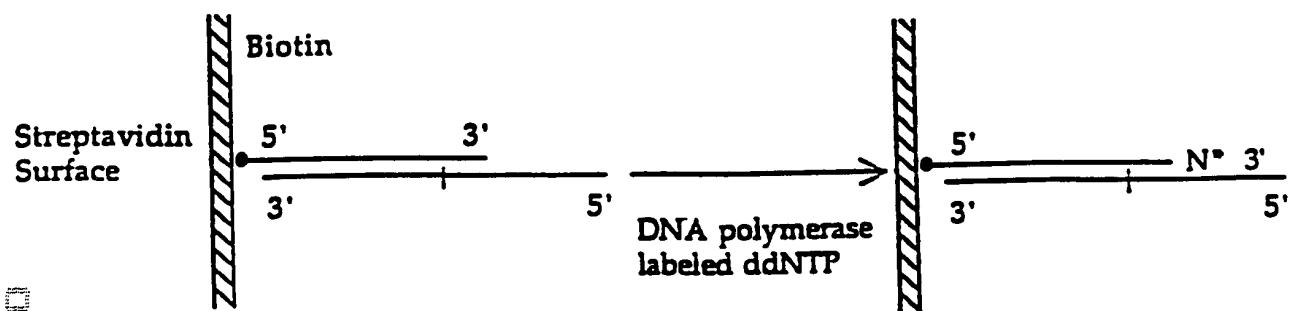
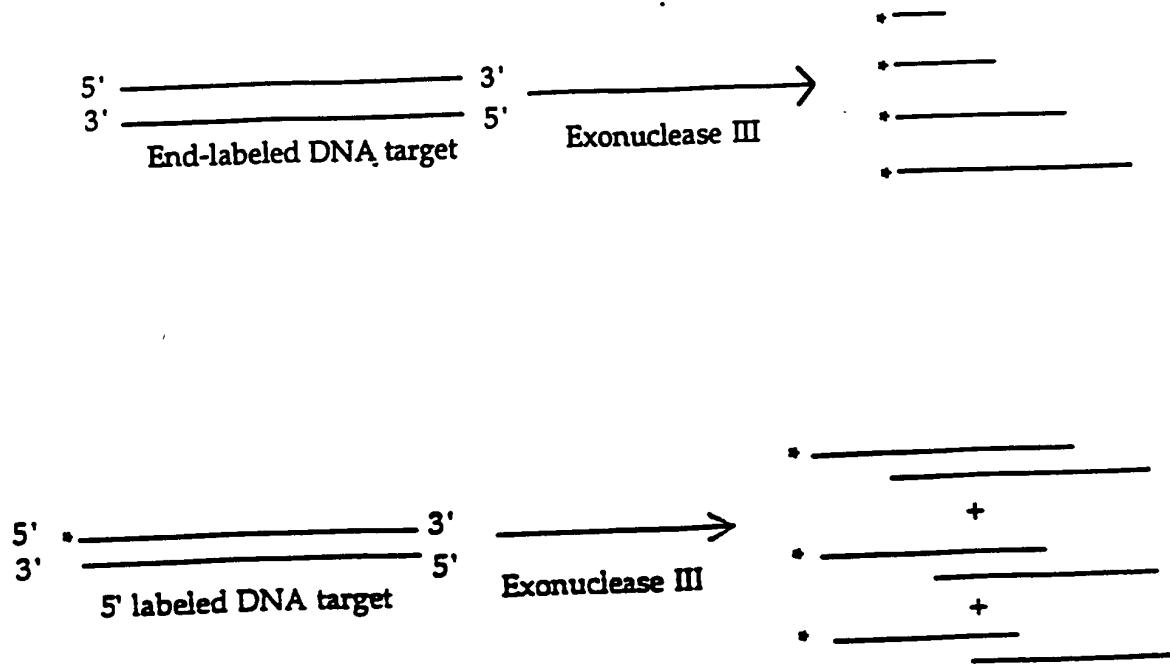


FIGURE 4



Reading an extra target base by 3' extension of the probe

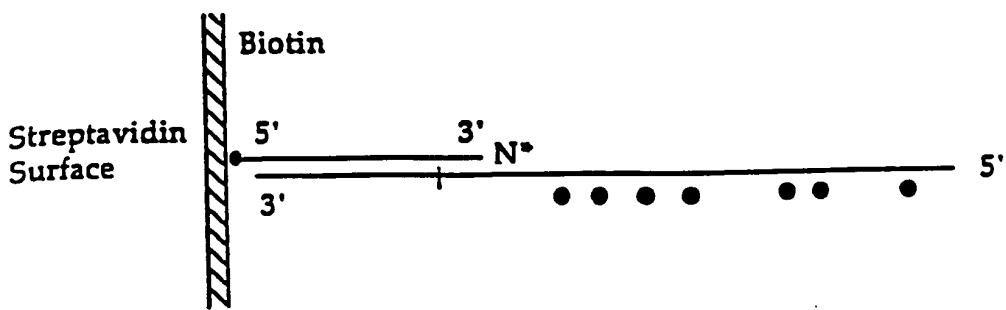
FIGURE 5



Preparation of a nested set of DNAs

09030624 02244620

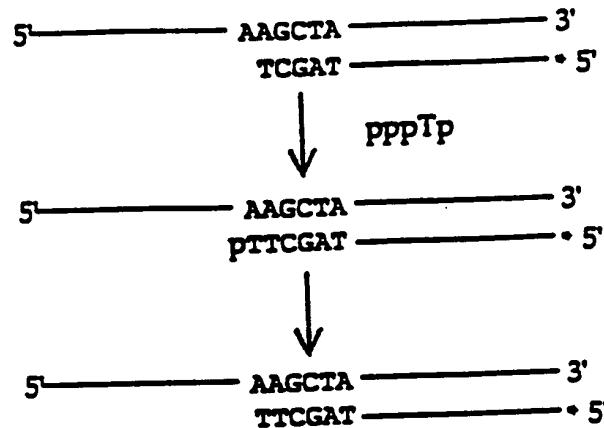
FIGURE 6



Positional information from ratio of internal label (●) to extension label (*). A 5' label could also be used.

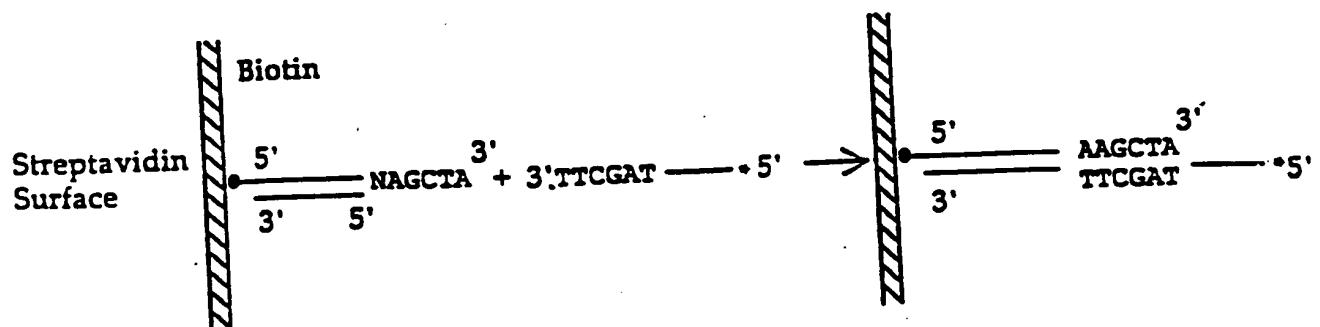
FIGURE 7

Reading an extra target base



Extension will fail with pppAp, pppGp, and pppCp

A. 3' extension of the target with a pppNp prior to phosphatase treatment



Array with one degenerate base

B. Hybridization and ligation

FIGURE 8

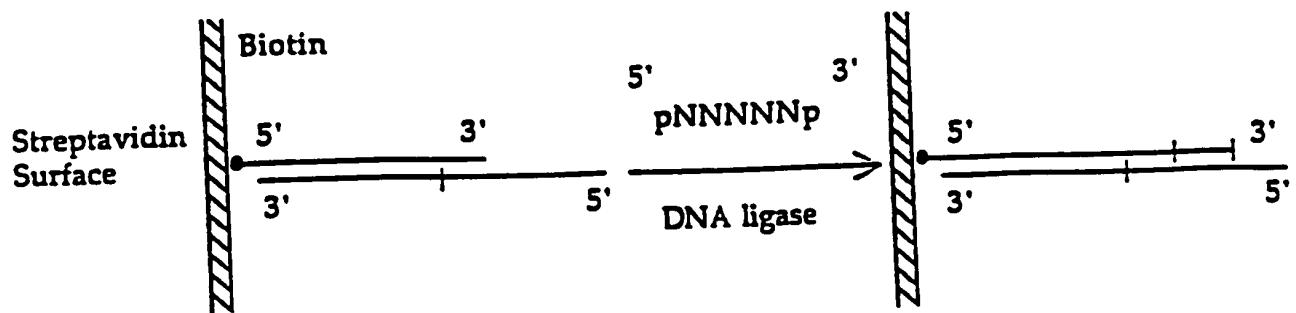
LABEL INTENSITY

Chain Terminator:	T	G	A
SEQUENCE			
GGAAT	2A, 2G	-	2G
AAGGT	2A, 2G	2A	-
GAAGT	2A, 2G	-	1G
AGGAT	2A, 2G	1A	-
AGAGT	2A, 2G	1A	-
GAGAT	2A, 2G	-	1G
GGGAT	1A, 3G	-	3G
GGAGT	1A, 3G	-	2G
GAGGT	1A, 3G	-	1G
AGGGT	1A, 3G	1A	-
AAAGT	3A, 1G	3A	-
AAGAT	3A, 1G	2A	-
AGAAT	3A, 1G	1A	-
GAAAT	3A, 1G	-	1G
GGGGT	4G	-	1T, 4G*
AAAAT	4A	1T, 4A*	-

Four color analysis of sequence extension of the 3' end of the probe. Label intensity shown does not include contribution from the 3' terminator.

* Plus additional possible residues

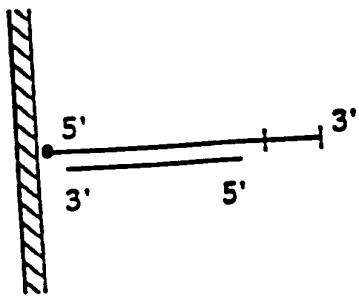
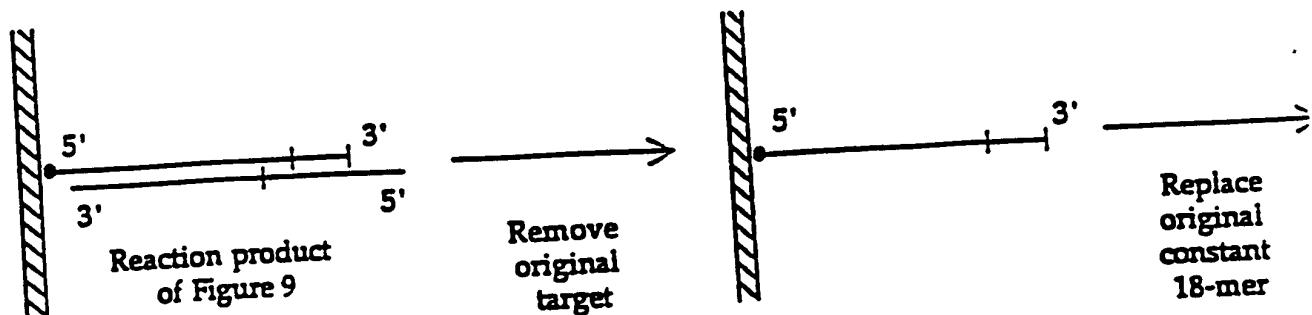
FIGURE 9



Extension of the probe by ligation of a blocked pentanucleotide.
The pentanucleotide is 3'-blocked to prevent polymerization.

FIGURE 10

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Preparation of a customized probe containing a 10 bp sequence present in the original target DNA

FIGURE 11

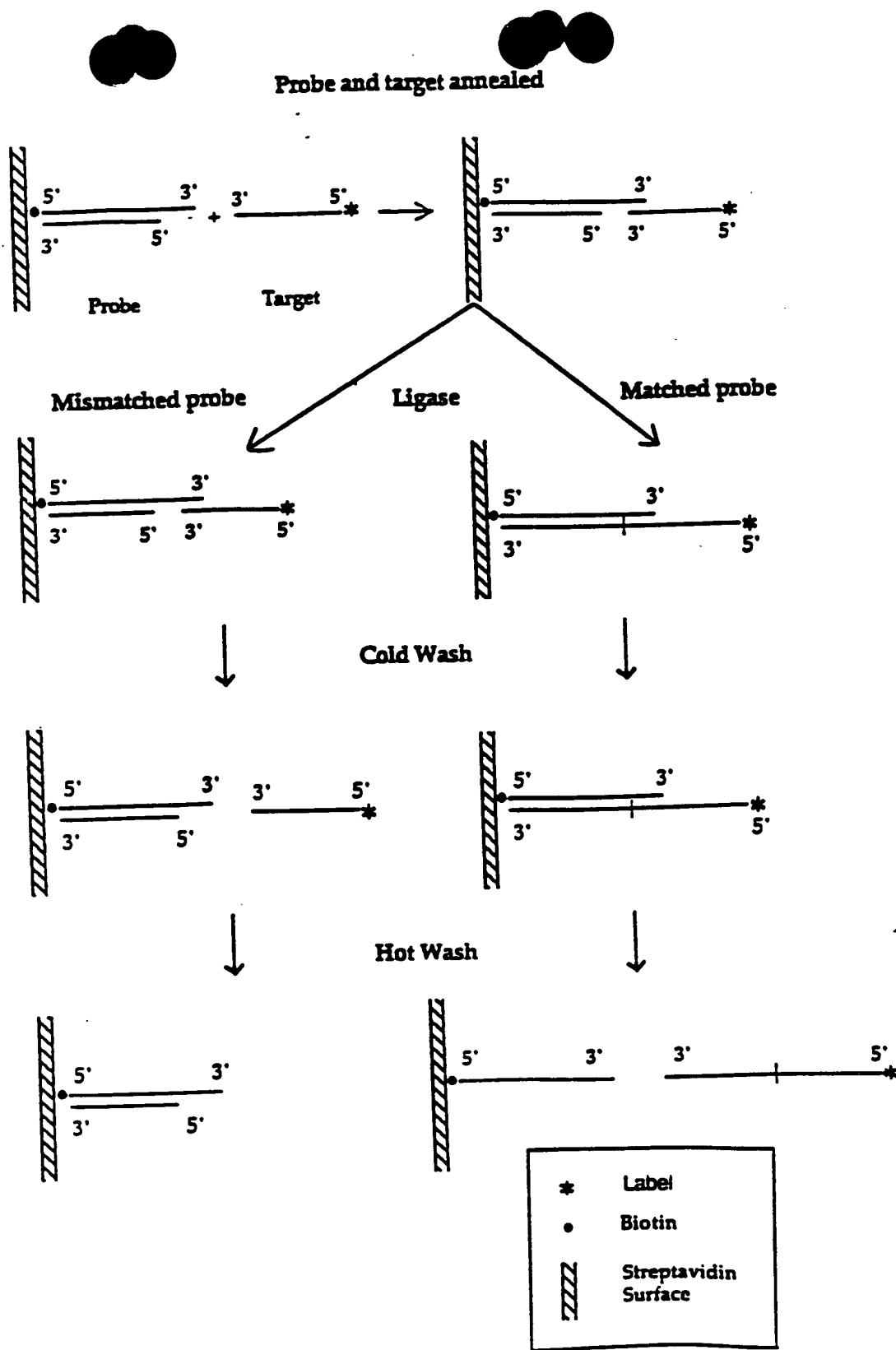


FIGURE 12

Ligation Efficiency

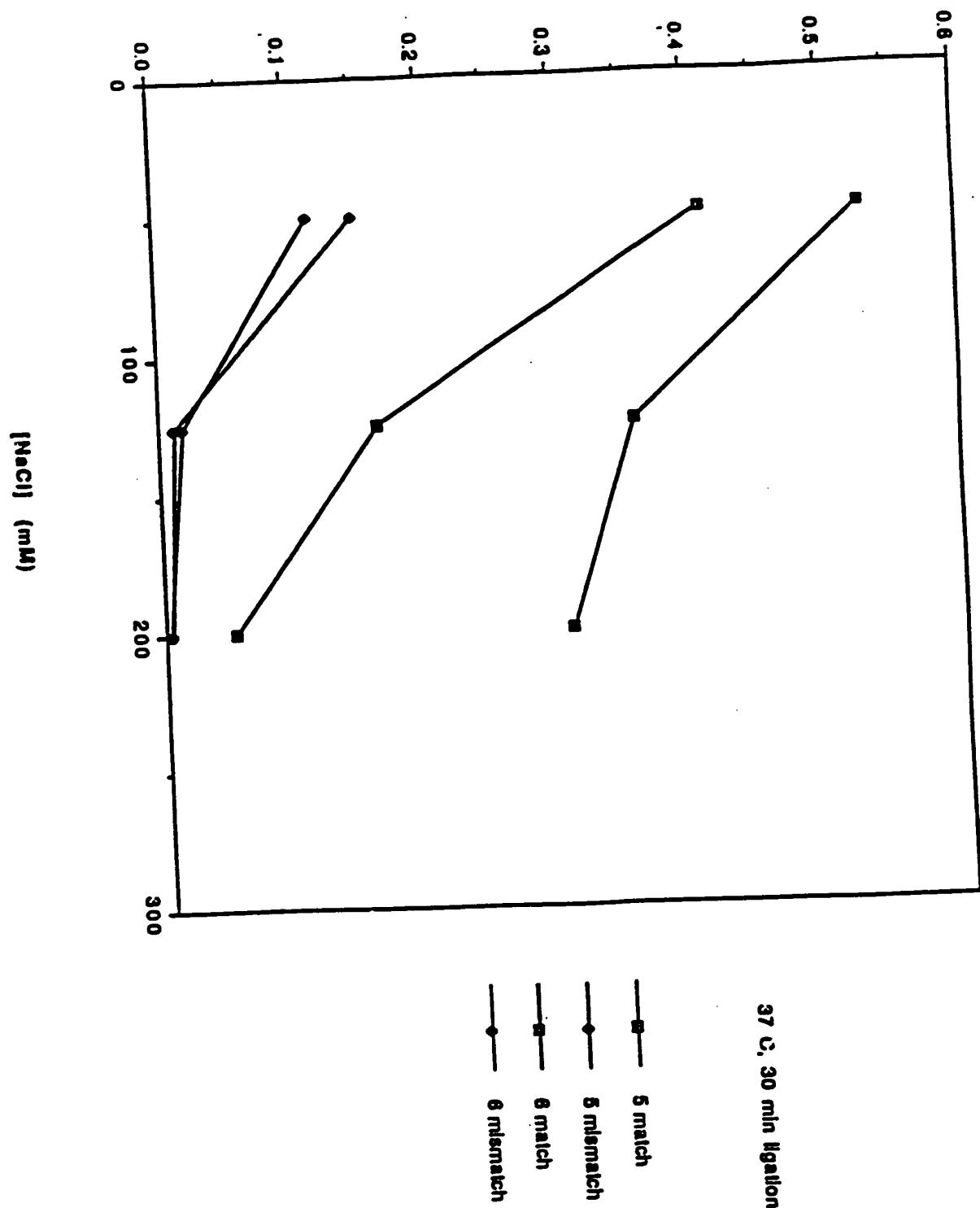


FIGURE 13

000000000000000000000000

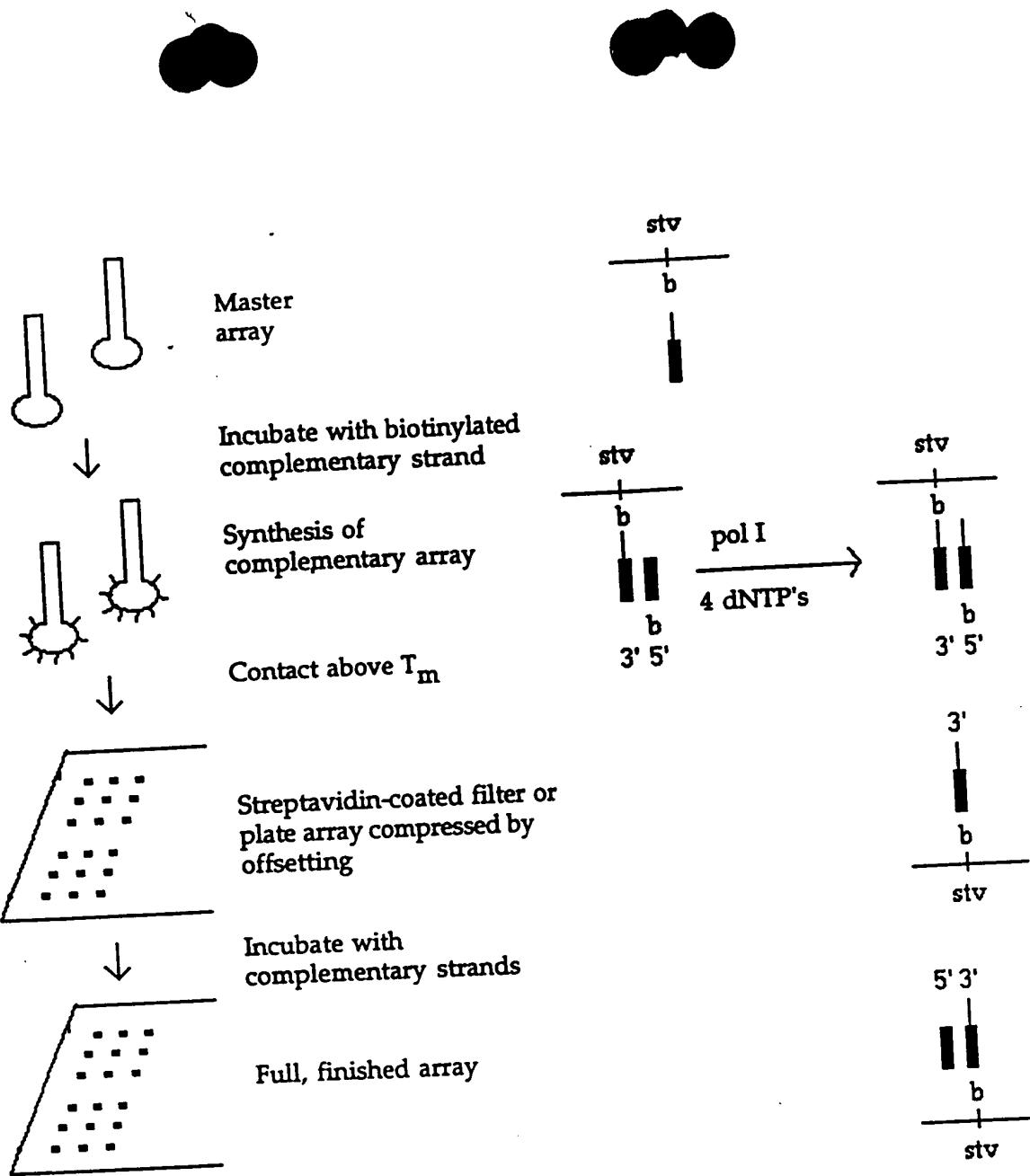


FIGURE 14